

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Run on:      May 18, 2002, 02:17:21 ; Search time 733.22 Seconds
              (without alignments)
              2528.938 Million cell updates/sec
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Title: US-09-719-748-1_COPY_62_1141
Perfect score: 1080
Sequence: 1 atgagcattcaagcagca.....ggagagagagcagcacttc 1080
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Searched:      1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1080	100.0	1742	21	AAZ49765	Human DAP-Kinase
2	1012	93.7	1253	23	BA573461	DNA encoding novel
3	516.2	47.8	2079	22	AAK94258	Human full-length
4	514.6	47.6	2132	20	AAK34656	Human ZIP-Kinase (
5	514.6	47.6	2224	22	AAH16158	Human cDNA sequen
6	514.6	47.6	2224	22	AAH78068	Nucleotide sequen
7	512.8	47.5	1459	20	AAK36657	Murine ZIP-Kinase
8	448.6	41.5	5862	16	AAO89839	Human death associ
9	448.6	41.5	5866	16	AAO89838	Human death associ

10	448.6	41.5	5886	19	AAV60289	DNA sequence encod
11	445.4	41.2	480	21	AAZ99730	CDNA encoding huma
12	445.4	41.2	1864	21	AAZ99730	CDNA encoding huma
13	385	35.6	757	22	AAK31856	Human CDNA 5'-end
14	385	35.6	757	22	AAK33262	Human CDNA clone r
15	244.6	22.6	12638	22	AAK70641	Human Immure/haema
16	238.4	22.1	1120	22	ABA09608	Human bone marrow
17	238.4	22.1	1502	22	ABA09692	Human bone marrow
18	202.8	18.8	3192	21	AAFL6067	Human prostate can
19	189.8	17.6	539	22	AAH06178	Human CDNA clone (
20	187.2	17.3	876	22	AAH46902	CDNA encoding huma
21	177	16.4	1773	22	AAAF4679	Novel protein kina
22	167.8	15.5	3262	23	ABL03417	Drosophila melanog
23	166.8	15.4	3284	23	ABL03403	Drosophila melanog
24	166.8	15.4	3374	23	ABL11987	Drosophila melanog
25	165.8	15.4	1836	22	AAAS6721	Polynucleotide seq
26	165.8	15.4	2046	22	AAH78263	Nucleotide sequenc
27	165.8	15.4	2671	22	AAAF46570	Novel protein kina
28	164.2	15.2	1839	24	AAAD65573	Human POLY4 CDNA
29	164.2	15.2	2625	22	AAAF4661	Novel protein kina
30	164.2	15.2	5532	20	AAZ25100	Human ischaemic he
31	163.4	15.1	3864	22	AAAF4664	Novel protein kina
32	163.4	15.1	5355	20	AAH89220	Seq ID NO: 28 of W
33	163.4	15.1	5355	20	AAH89220	Seq ID NO: 30 of W
34	163.4	15.1	5355	21	AAZ39404	Human Ttrad protein
35	163.4	15.1	5355	21	AAZ39405	Human Ttrad protein
36	162.8	15.1	1971	24	AAAD6571	Human POLY3 CDNA
37	162.8	15.1	2558	24	AAAD6572	Human POLY3 CDNA
38	161.4	14.9	1917	23	ABLO3333	Drosophila melanog
39	154.6	14.3	2973	24	AAAD6453	Human foetal PKIN
40	154	14.3	513	22	AAAB0648	Human foetal liver
41	154	14.3	513	22	ABAA28854	Probe #7320 for ge
42	154	14.3	513	22	AAK09135	Human brain expres
43	154	14.3	513	22	AAK35024	Human bone marrow
44	154	14.3	513	22	AAI16902	Human bone marrow
45	154	14.3	513	22	AAI40741	Probe #6835 for ge
					Probe #9427 used t	

## ALIGNMENTS

```

RESULT      1
AAZ49765
ID   AAZ49765 standard; DNA; 1742 BP

```

AC - AA249765;  
XX  
DT 18-APR-2000 (first entry)  
..

Human DAP-kinase-related protein 1 (DRP-1) encoding DNA

KM DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;  
KM cyclodulin-dependent serine/threonine kinase; apoptosis; tumourisation;  
KM cytosolic; antipsoriatic; immunosuppressive; metastasis; human  
KM treatment; cancer; psoriasis; autoimmune disease; screening; ds.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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FT      /product= "DAP-kinase-related protein 1"
FT      polyA_signal
FT      1720..1725
FT      /*tag= b
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PN W09966030-A1

PD 23-DEC-1999.

PF 15-JUN-1999;

PR 15-JUN-1998; 98US-0089294.

PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (MCIN/) MCINNIS P A.  
 XX  
 PI Kimch1 A;  
 XX WPI: 2000-147148/13.  
 DR P-PSDB: AAY44674.  
 XX  
 PT Calmodulin-dependent serine/threonine kinase capable of inducing  
 PT apoptosis used in the treatment of e.g. cancer -  
 XX  
 PS Claim 3; Fig 1; 67pp; English.  
 XX  
 CC The present sequence encodes DAP (death-associated protein)-  
 CC kinase-related protein 1 (DRP-1), which is a calmodulin-dependent  
 CC serine/threonine kinase. DRP-1 is a cytoplasmic protein capable of  
 CC inducing apoptosis by dimerisation. It shows significant homology to  
 CC DAP kinase. It has cytosolic, antiproliferative and immunosuppressive  
 CC activity and can be used for inhibiting growth/metastasis of  
 CC tumours and promoting death of tumour cells. It can also be used in  
 CC the treatment of cancer, psoriasis and autoimmune diseases. Fragments  
 CC of DRP-1 DNA are useful as probes for screening individuals with a  
 CC predisposition to cancer.  
 CC  
 SQ Sequence 1742 BP; 442 A; 437 C; 504 G; 359 T; 0 other:  
 Query Match 100.0%; Score 1080; DB 21; Length 1742;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-289;  
 Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 62 atggaagcattcaagcagcagaagtgaggactttatgacatcgagaagagctggg 121  
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 Db 122 agtggcagattccatcgtaagaagtgccggagagaagcaggggcttgatgca 181  
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 Db 182 gccagttcatcaagaagcggcagagccggcgccggcggtgtgagccggaggag 241  
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 Db 242 atcgagcggggagtgagcattccctgcgcaagtgctgcaccaaagtcatcagctgcac 301  
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 QY 301 ctcttcgattcccgcccaagaagagtcactgagtgaggagggccacacgcttcatt 360  
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 Db 362 ctcttcgattcccgcccaagaagagtcactgagtgaggagggccacacgcttcatt 421  
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 QY 421 aagcagaaacattatgtgtttagacaagaatattccattccacataaagctgatt 480  
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Db 662 ttgagcatggcgctacatcctccttaagtgtgagacatcccttctctggagagc 721  
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RESULT 2  
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 ID AAS73461 standard; CDNA: 1253 BP.  
 XX  
 AC AAS73461;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #9265.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001/5067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001: 2001WO-US08631.  
 XX  
 PR 31-MAR-2000: 2000US-0540217.  
 PR 23-AUG-2000: 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YF;  
 XX  
 DR WPI: 2001-639362/73.  
 DR P-PSDB: ABG09274.  
 XX  
 PT New isolated polynucleotide and encoded polypeptide, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 PS  
 PS Claim 1; SEQ ID No 9265; 103pp; English.  
 CC  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The

polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/pct\\_sequences](http://wipo.int/pub/pct_sequences).

**SQ** Sequence 1253 BP; 331 A; 303 C; 366 G; 253 T; 0 other;

Query Match	93.78;	Score 1012;	DB 23;	Length 1253;
Best Local Similarity	99.58;	Pred. No. 2e-270;		
Matches 1015; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0

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QY	181	atcgagcgaggagctgtgaagcatctctgcggcagagtgtctgcacacaaatgcatcaacgtcgac	240
Dp	351	atcgagcgaggagctgtgaagcatctctgcggcagagtgtctgcacacaaatgcatcaacgtcgac	410
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QY	421	aagcagagaaaaatactatgtctgttaagacaagaaatctccatctccacacatcaagctgatt	480
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QY	481	gaactcttgcttgagcctcagaagaaatagaagaatggaagtgtgaaatlaagaatacttttggagag	540
Dp	651	gaactcttgcttgagcctcagaagaaatagaagaatggaagtgtgaaatlaagaatacttttggagag	710
QY	541	ccggaatctgtctgcctccagaaaaatctgtgaactacggagccctctggctctgaagagctgaacag	600
Dp	711	ccggaatctgtctgcctccagaaaaatctgtgaactacggagccctctggctctgaagagctgaacag	770
QY	601	tggagacataagcgtctcatcaactcaatcctcttaagtgtgaagcatccctctctctggagagac	660
Dp	771	tggagacataagcgtctcatcaactcaatcctcttaagtgtgaagcatccctctctctggagagac	830
QY	661	acgaaagcagaaacacctgtgacaatatcacaatcaagtgagatctgaagactcttgatagagaaac	720
Dp	831	acgaaagcagaaacacctgtgacaatatcacaatcaagtgagatctgaagactcttgatagagaaac	890
QY	721	ttcagcatcaagcagcgaagctgtgcacaaagaaatttatctggaaagctctctgttlaaagagacc	780
Dp	891	ttcagcatcaagcagcgaagctgtgcacaaagaaatttatctggaaagctctctgttlaaagagacc	950

Qy	781	cgagaaacggtctcaataccaaagaggtctctcagacaccccttgatctaacgcggtgagaaac	840
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Qy	841	cagaaacgcatactgtgcgacgagatctgtgctaatctctgaagaactctcaagaaacagat	900
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RESULT	3
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ID	AAK94258 standard; cDNA; 2079 BP.

AC AAK94258;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human full-length cDNA, SEQ ID NO: 2874.  
 XX  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PE 07-JUL-2000; 2000EP-0114089.  
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 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
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 PA (HELI-) HELIX RES INST.  
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 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI; 2001-524255/58.  
 DR P-PSDB; AAM93338.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 2874; 1380bp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SEQ Sequence 2079 BP; 396 A; 626 C; 733 G; 324 T; 0 other;





OY 781 cggaaagcgtcacatccaaagagctctcagacacccctgatacgcggt 833  
 Db 995 aagcggagaatgacatctgcacagagcctcggaaacattccgtatgaagcgat 1047  
 RESULT 6  
 AAH78068 standard: DNA: 2224 BP.  
 ID AAH78068 standard: DNA: 2224 BP.  
 XX  
 AC AAH78068;  
 XX  
 DT 26-NOV-2001 (first entry)  
 DE Nucleotide sequence of a human protein kinase/protein phosphatase.  
 XX  
 KW Human; protein kinase; protein phosphatase; signal transduction;  
 XX intracellular signalling pathway; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 215..1579  
 FT /tag="a"  
 FT /product="protein kinase/protein phosphatase"  
 XX  
 PN MO200109345-A1.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PE 28-JUL-2000; 2000MO-JP05060.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 PR 18-OCM-1999; 99US-0159590.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 17-FEB-2000; 2000US-0183322.  
 PR 02-MAY-2000; 2000JP-0183767.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
 PI Senoo C, Nezu J;  
 XX  
 DR WPI: 2001-564736/63.  
 DR P-PSDB: AAG67425.  
 XX  
 PT New genes encoding protein kinase and protein phosphatase, useful for  
 PT identifying modulators which can be used to treat human or animal  
 PT disorders associated with the expression or function of these enzymes -  
 XX  
 PS Claim 1; Page 119-125; 336pp; Japanese.  
 XX  
 CC The present sequence encodes a human protein kinase/protein  
 CC phosphatase. The polypeptides are expected to participate in signal  
 CC transduction in cells. The kinase phosphatases are connected with  
 CC intracellular signalling pathways. Antisense oligonucleotides and  
 CC compounds identified by screening (agonists or antagonists) can be  
 CC used to treat human or animal disorders associated with the expression  
 CC or function of the protein. In addition, the polypeptides may be used  
 CC as target molecules for drug development.  
 XX  
 SO Sequence 2224 BP; 419 A; 656 C; 806 G; 343 T; 0 other:  
 Query Match 47.6%; Score 514.6; DB 22; Length 2224;  
 Best Local Similarity 76.1%; Pred.No. 2.4e-137;  
 Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;  
 OY 1 atgagacattcaagcagaagtgtagactttatgacatcggagagagctgggg 60  
 Db 215 atgtcacgttcagcagagagcgtgtagaccattatgagatgagagagctgggc 274

OY 61 agtggccaatttgcctatcgtgaagaagtgccgggagagaagcacggggcttgatgcga 120  
 Db 275 agcggccaagtttcgacatcgtgaggaagtgccgggagagaagggcacgggagtgacgca 334  
 OY 121 gccaaatctcaacaaagacggcgacagagccggcgagctgtgagccgggagagag 180  
 Db 335 gccaaatctcaacaaagacggcgacatccacagccggcgctgggtgtagccgggagagag 394  
 OY 181 atcgagcggagagtgagatctctgcgcagagtgctgcacacaaatgtatcacgctgac 240  
 Db 395 atcgagcggagagtgagatctctgcgcagagtgctgcacacaaatgtatcacgctgac 454  
 OY 241 gacgtctatgagaacccgacagcagctgtgacatctcttgagctagtgctgcgagagag 300  
 Db 455 gacatctcggagaacaaagacagctgtgcttcacatccctggagctgtctcggcgagag 514  
 OY 301 ctcttgatcttcggcccaagaagagtcacatctgagtgagtgagagagccacacgctcat 360  
 Db 515 ctcttgatcttcggcgagagagagtgctgcagcagagagccacacgctcatcctc 574  
 OY 361 aagcagatctcgtgagtgagtgagtgacatctcaccacaaagaatgtctcatctgactc 420  
 Db 575 aagcagatctcgtgagtgagtgagtgacatctcaccacaaagaatgtctcatctgactc 634  
 OY 421 aagcagaaacataatgtgttgtagaagaatattccatccacacatacagctgatt 480  
 Db 635 aagcagaaacataatgtgttgtagaagaatattccatccacacatacagctgatt 694  
 OY 481 gactctgctcgtgcacagaaatagagaatgagtgagtgaaatlaagaatattttggagcg 540  
 Db 695 gactctgctcgtgcacagaaatagagaatgagtgagtgaaatlaagaatattttggagcg 754  
 OY 541 ccggaatttgctgcacagaaatgtgaaatcagagcccttggtcttgagagctgacatg 600  
 Db 755 ccggaatttgctgcacagaaatgtgaaatcagagcccttggtcttgagagctgacatg 814  
 OY 601 tggagcattagggctcatcactacatcactccttaagtgagagcattccctctcggagagc 660  
 Db 815 tggagcattagggctcatcactacatcactcctcctcagagcgtgacatccctctcggagagc 874  
 OY 661 acgaagaagaaacactgycacaaatatacacaatcagatgagtgaaacttgatgagaaatcc 720  
 Db 875 acgaagaagaaacactgycacaaatatacacaatcagatgagtgaaacttgatgagaaatcc 934  
 OY 721 ttcaagcattcagagcagctgagcctgccaagagcttatttcggagagcctctgtgttaagagac 780  
 Db 935 ttcaagcattcagagcagctgagcctgccaagagcttatttcggagagcctctgtgttaagagac 994  
 OY 781 cggaaagcgtcacatccaaagagcgtctcagacacccctgatacgcggt 833  
 Db 995 aagcggagaatgacatctgcacagagcctcggaaacattccgtatgaagcgat 1047  
 RESULT 7  
 AAX34657 standard: DNA: 1429 BP.  
 ID AAX34657 standard: DNA: 1429 BP.  
 AC AAX34657;  
 XX  
 DT 01-JUL-1999 (first entry)  
 DE Murine ZIP-kinase (serine/threonine kinase) encoding, DNA.  
 XX  
 KW Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;  
 KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;  
 XX Human; murine; ss.  
 OS Mus musculus.  
 XX  
 PN EP911408-A2.  
 PD 28-APR-1999.



Sequence 4272 BP; 1076 A; 1161 C; 1121 G; 914 T; 0 other;  
xx  
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Best Local Alignment	0	Mismatches	294	Indels	24	Gaps	14
Matches	659	Conservative					

QY	10	ttcaacgacgcaagaagctcgtgaggaacttctatgcatactgaaagagcgctgagggaattggccag	69
Db	10	ttcagagcaggaacacgtcgatgatatctctccgacaccggtcgaggaactcttgaaatgtgacag	69
QY	70	tttgcacatcgtgaagaagctgcggtgaggaagagacacggtggtctgtgaattatgcagccaagtcc	129
Db	70	ttctggtgtgtgaaagaaatgcgtgtgaaanaagtaccggctccacgttatcccgccaattc	129
QY	130	atcaagaagcgtgcagaagccgtgacggtgcgtgtgtgagccgtgaggaagaaatcgtgaacgtg	189
Db	130	atcaagaaaaggagagactcaatgtccagcgtggtgtgtgagccgtgaggaagaaatcgtgaacgtg	189
QY	190	gaagctgagcattccctcgtgcaggtgtctgcacacaaatgatacagctccacacgaactcat	249
Db	190	gaagtctagaactctgaagagaaatcccaagaccaccaatgatacacccttcagacgaagctcat	249
QY	250	gaaacaacgcacacgaactgtgtgcatactcttgagctagtgtctgagagagactcttcgat	309
Db	250	gagaaacaagaacggaactcactcctgtgactctgtgaactcgttgacagttgtgcaggtgtgttttgc	309
QY	310	ttccctgtgccagaagagatcactgtgagtgaagagagagccacgaagctcaattgaagacatc	369
Db	310	ttctctagctgaanaaggaactcttaactctgaagagagaaacgaactgaattctccaacaactt	369
QY	370	ctgtagatggtgtgaaactacttcacacaagaagaaattgcactcttgatctcaagccagaat	429
Db	370	cttaaatgtgttactaactctgcataccctctcaaatcgcacacttgatctcttaagccctgag	429
QY	430	aacatactgttgttaagacaagaatatcccatctccacatccaagctgaattgttcctt	489
Db	430	aaactaatgtctttgtgatalagaaatgtccccaacacctgtgacataagaatcatttgact	485
QY	490	ctgtgctacgaataatagaagatgtgagtgtgaatttaagaatatcttttggagacgcggaatt	549
Db	490	ctgtgctacgaataatagaagatgtgagtgtgaatttaagaatatcttttggagacgcggaatt	549
QY	550	gttgcctccagaatctgtgaactacgcgacccctggtgtcgtgagctgtgacatgtgtgagcata	609
Db	550	gttcgctctctgtgatalagccaactatgaaacctgtgtctgtgagcgagatgtgtgagatc	585
QY	610	ggcgtcacactacatcctctctaagtgtgagcatccctcttcctcttggtggagaaacgaacg	669
Db	610	gggtgataataacatctatcctctctaagtgtgaggtccctcccaattctctgtgagaactaagcaa	645
QY	670	gaaacactgtgcaaatatcacatacgaatgtgagtgtgacgaactgtgagaggaattcttcagcat	729
Db	646	gaaacgttttagcaaaatgtatccgctgtcaactactgaattgtgagatgtgaattactgaat	705
QY	730	acgagagagctgtgcacaagaagacttatctcgaaagctctcgtgttaagagacccggaacg	789
Db	706	acaaagtcctctagccaagaattctcataagaagctctcgtgtcaagagatccaagaagagaga	765

Db 946 tccgaagtaacatgag 962

AAQ89838  
ID AAQ89838 standard; cDNA; 5886 BP

04-JAN-1980 (first entry)

XX Death associated protein; DAP; cytokine; cell death; ss

	Key	Location/Qualifiers
XX		
FH		

FT CDS 33/..4605  
/\*tag= a

FT 5628.5633

FT	polyA_signal
5855.	.5860

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FT misc_feature 5114..5118
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feature  
5103. 5107  
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ET	/cug
ET	/label= instabilit

AA  
PN W09510630-A.

PD 20-APR-1995.

PF 12-OCT-1994; 94WO-0511350.

PR 12-OCT-1950  
XX

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Kimchi A;

DR WPI; 1995-1/8528/23.  
DE P-PSDB: AAR74205.

DNA whose expression mediates cyto

uncontrolled, pathological cell growth

XX English

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XX  
XX

DAD comes seem to play an imp. ro

CC inhibition of cell death. A CDNA library  
CC promoted cell death.

CC promoted cell death. A cDNA library was generated from



mRNAs harvested after treatment of Hela cells with IFN- $\gamma$ . It was cloned in antisense orientation into the EBV-based pTK01 expression vector. The resulting expression library was introduced into HeLa cells. A fraction of the transfectants was selected with hygromycin B. The majority of transfected cells were selected with both hygromycin B and IFN- $\gamma$ . The cells that survived and/or grew in the presence of IFN- $\gamma$  were expanded and pooled. The extrachromosomal DNA was obtained and cleaved with DpnI and introduced into E. coli HB101 host cells. A few bacterial clones were obtained which included DNA antisense sequences, some of which were able to protect cells from the death-promoting effects of IFN- $\gamma$ . Plasmid DNAs were prepared from 10 individual bacterial clones. PCR amplified cDNA inserts were generated from each plasmid using primers that correspond to the immediate flanking sequence of the cDNA insertion sites in the pTK01 vector. The PCR fragments were used as labeled probes to search Southern blots for possible cross hybridisation between some of the rescued antisense cDNA clones. The 10 cDNA clones were classified into six distinct non-overlapping groups, some constituting several members (clones) and some constituting a single member. Antisense cDNA clone 256 has the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and used to screen a K562 lambda gt10 cDNA library. The resulting composite sequence derived from 2 clones and the deduced AA sequence are shown in AA089838 and AA074205. The ORF is also shown in AA089839. AA089838 has a poly A tail. The calculated mol. wt. of the protein is about 160 kDa. Several known domains and motifs were identified in the protein (see AA074205 FTY).

SQ Sequence 5886 BP; 1447 A; 1524 C; 1500 G; 1415 T; 0 other;

Query Match	41.58;	Score 448.6;	DB 16;	Length 5886;
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Best Local Similarity 67.5%; Pred. NO. 7.7e-114;  
Matches 659; Conservative 0; Mismatches 294; Indels 24; Gaps 1

OY	10	tttaagacgacgaagagctgtagaacttttatgtacattcggagagagcgctcgaggagtgtgcacg	69
Db	346	ttcaagtcagtgaaaacacgtgtgatagtatctacacacgaccccgcgagaaactcttgccagctgtagac	405
OY	70	ttctgcatactgtaaaagatctgcacgggagaaagacacggcggtctgtgatactgacgccaagtctc	129
Db	406	cttggtgtgtgtgaaagaaatctgcgtgagaaagatcccgctccacgtatctcccgccaacttc	465
OY	130	attcaagaaagcggacagagccgggcgagccgcgcggtgtgtgacccggagagatccgagccgg	188
Db	466	attcaagaaagaaagagagatctcaaaatccacagccgggtgtgtgagccgagagacatccgacg	525
OY	190	gaggtggaacatctccgctcgacgagtgctctgcacacaaatctaatcaagacgcgacagatctat	249
Db	526	gaggtgtcagcatctcgtgaagagaaatccaaagaaaccccaatgtcatcacaccccgacagatctat	585
OY	250	gagaaacccgacacgcgaactgtgtgtacatcccttgagctatgtctgtgagagagagctcttcgat	309
Db	586	gagaaacaaagacggaacgctatccatctgtactgtgaaactcgtctgcaggttgccgagctgttgac	645
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Db	646	tctctaaagcttgaaaagagaaatcttctaacctgtaaaagagaaacaaatctgaattctcaaaaacaaat	705
OY	370	cttgagatgtgtgaaacacacatccacacaaagaaatctgcactctgtatcttcaaacgaa	429
Db	706	ctttaaigtgtgtactactacctgcactcccttcaaatctgcacacttgtattcttaagcccgag	765
OY	430	aacatctatgtgtgttagacaagaataatcccatctccacacatcaagctgattgactgtgt	488
Db	766	aacataaagctctctgtgataagaaatgtccctccaaacactcgtgataagaatcatcttgact---	821
OY	490	cttggtctacgtaataagaaatctgaggtctgaacttaagaatatctttgtgagccggaatt	549
Db	822	-----ctgaaatggaattcttaaaaaacatatcttggatctccgaagtt	601
OY	550	gtctgctcagaagaattgtgaactaagagccctctggtctctgagagctgtgacatgtgtgagata	609

[illegible]

RESULT 10

ID AAV60289 standard; DNA; 5886 BP.

AC AAV60289;

DT 12-JAN-1999 (first entry)

DE DNA sequence encoding death associated protein-2 (DAP-1, DAP-kinase).

KW Death associated protein; DAP-2; cell death; tumour cell; DAP-kinase;

KW programmed cell death; degenerative neurological disease;

•

XX

FT	CDS	337.4608
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FT /product= DAP-2

PN W09839429-A2

PD 11-SEP-1998.

PF 03-MAR-1998; 98WO-IL00102.

PR 03-MAR-1997; 97US-0810712.

PA (YEDA ) YEDA RES &amp; DEV CO LTD

PI Kimchi A;

DR WPI; 1998-520781/44.

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PT diagnosis and treatment or disorders associated with programmed cell death or cancer, autoimmune diseases or neurological diseases

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Sequence 5886 BP; 1447 A; 1525 C; 1499 G; 1415 T; 0 other;

Matches	659;	Conservative	0;	Mismatches	294;	Indels	44;	Gaps	1
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Db 1042 accagtgccttagccaaagatttcataagaagactctcgtgcagaagcaccacaagayayg

Db 1282 tccagaagtaacatgag 1298

AAZ99731  
ID AAZ99731 standard; cDNA; 480 BP

AAZ99731;

DT 12-JUL-2000 (first entry)

XX cDNA encoding human cardiovascular system associated protein kinase-4.

XX  
KW  
Human: cardiovascular system associated protein kinase-4; CSAPK-4;

signalling pathway; cell growth; cell  
tissue typing; forensic identification; cardiovascular disease;  
KW

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KM  
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congressive health insurance

OS Homo sapiens.

Key	Location/qualifiers
1	480

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/*tag= a
/product= " cardiovascular system associated protein

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FT kinase-4

PN WO200014212-A1

PD 16-MAR-2000.  
XY

PF 09-SEP-1999; 99WU-US2003L  
YY

PR	09-SEP-1998;	98US-003502/
PR	29-SEP-1998;	98US-0163115

XX  
PA (MILL-) MILLENNIUM PHARM INC.XX  
PI Acton SXX WPI; 2000-271053/23  
DR

DR P-PSDB, AN104220  
XX

new nucleic acid staining, treatment and prevention of PT kinase, used e.g. for diagnosis,

F1	CALCULOVADO	1978-1979	Feet
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protein kinase-4 (CSAPK-4). CSAPK polypeptides are involved in signaling pathways that regulate cell growth and differentiation. The CSAPK

polypeptides and polynucleotides are used to screen for agents that regulate CSAR, which are potential therapeutic agents.

They are also used for diagnosis, prognosis or monitoring of gene mapping, tissue typing and forensic

Identification, and for treating or preventing disorders associated with abnormal gene expression or activity, especially cardiovascular

diseases such as congestive heart failure. They can also be used in the CSAPK polynucleotide may also be used to generate





CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
CX  
XX  
Sequence 757 BP: 176 A; 219 C; 220 G; 133 T; 9 other;

Query Match	35.6%	Score 385;	DB 22;	Length 757;
Best Local Similarity	75.6%	Pred. No. 1.3e-96;		
Matches 511; Conservative	0;	Mismatches 162;	Indels 3;	Gaps 3;

OY	1	atgagagcattcaagacgagaaagctgagagactttatgacatcggagagagcgctggg	60
Db	70	atgtccaaagctcaagcagcagaaacgcttgagagccattatgagatctggggagagcttgggc	129g
OY	61	agctggcaggtcttgccatcgtgtaaagctgcggggagagagagcagcggtcttgatgca	120g
Db	130	agcggcgcaggtcttgagatcgtgtcggaagtgcgcgcagaaagagcaacggtcaagagagatagca	189g
OY	121	gccaaatctcaacaaagaaagcggagaaagacgggacggagcggtgtgagccggaaag	180g
Db	190	gccaaatctcaacaaagaaagcggcgctctcatccagccggcggtgggctggagcggagag	249g
OY	181	atcgagcggggggtgagagcatctctgcgcagagtgctgtgacacaaatgtcatcaacgctgac	240g
Db	250	atcgagcgggggtgagaaatctctgcggagatcccgagaccacaaatcatcatcccttgcac	309g
OY	241	gacgtctatgagaaacgcgacacgaaagtgtgtgacatctcttgagctagtgcttgagagag	300g
Db	310	gacatctctcgagaaacagaaacgagacgtgtgtctctcatctctgagatgctgtctcttgcggggag	365g
OY	301	ctctctgattctcttgcggcccaagaaagatcaatcgagtgagagagagagagcacaatcat	360g
Db	370	ctcttgcattctccgtgcggagaaagagctgcgtgacgagagagagagcaccacaaatctctc	429g
OY	361	aagcagatccctcgatctgggtgagatctactcttcaaccaagaagaattgtctacttgaatc	420g
Db	430	aagcagatccctcgagacgggtctcatctctgacatcttaagcgcatactgcacacttgaacttg	489g
OY	421	aagcagaaacaaatcatatgtctgtagacaaagatactccatctccacatcaagctgatt	480g
Db	490	aagccggagaaacatcatatgctgtctgagaaagacgtgcacaaacagaaatcaagctatc	549g
OY	481	gacttggctctgctcagaaataagaaatgagatgaaatttaagaaatatcttcttggagcg	540g
Db	550	gactctgcgcacgcgcacaaagatcgaagcgggagaaatcaanaacatctctcgacac	609g
OY	541	ccggaa-cttctgtctcagaaatcttgaaactagagacccctgtgtc-tgagagctgaca	558g
Db	610	ccggaaattcttgcgcacaaaaatttgaaactagaaacgcgtggccttggacgttgaagcngaca	669g
OY	599	tgttgagataagcgctcatccatccatccctcttaagtgtgagat-ccctcttccctggga	657g
Db	670	tgttgaaacatcgtgtctccctctatccctcttgaaacggtgtgacccctcttccctgggc	729g
OY	658	gacacgaaagcagagaa 673	
Db	730	aaaaccaacnagana 745	
RESULT 15			
AAK70641			
ID	AAK70641	standard; DNA; 12638 BP.	
XX	AAK70641;		
DT	06-NOV-2001	(first entry)	
XX			
DE	Human	Immune/haematopoietic antigen genomic sequence SEQ ID NO:25453.	
XX			
KM	Human: Immune; haematopoietic; Immune/haematopoietic antigen; cancer;		
XX	cytostatic; gene therapy; vaccine; metastasis; ds.		
CS	Homo sapiens.		

[illegible]

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PI   Rosen CA, Barash SC, Ruben SM;
XX   WPI: 2001-483426/52.
XX   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX   useful for preventing, diagnosing and/or treating cancers and
XX   metastasis -
XX   Disclosure: SEQ ID NO 25453; 3071pp + Sequence listing; English.
XX   PS
XX   AA
XX   AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC   amino acid sequences given in AAK82170 to AAK91921. (I) have cytosolic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patient's own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/hematopoietic-related diseases, especially
CC   cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/hematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC   represent sequences used in the exemplification of the present invention.
XX   XX
XX   Sequence 12638 BP; 2397 A; 3383 C; 3994 G; 2864 T; 0 other;
S0

Query Match          22.6%; Score 244.6; DB 22; Length 12638;
Best Local Similarity 79.6%; Pred. No. 4.2e-57;
Matches 289; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY   61 agtggccagtttgcctatcgtagaagaagtgccgggagagaagacaggggcttgagtatga 120
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DB   6096 agcgcccggttggatcgatcgaggaatgctgcggagagaagcgacgggcaaggagtacga 6155

QY   121 gccaaattcatcaagaagaagcggagacggcggaagcgagcggtgtgagccggagagga 180
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DB   6156 gccaaagtcatcaagaagaagcggcgctgtcatcacagcggcggtggtgtgagccggagga 6215

QY   181 atcgaagcggaggtgtagatcatctcgagcagggtgtgtcacaccacaatgtcatcaagctgcac 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   6216 atcgaagcggaggtgtgaaatcatctcggtggagatccggcacccacaatcatcaaccctgcac 6275

QY   241 gacgtctatagaacccgacccgaagctgtgtgcacatccttgagcctgagttgtgtgagagga 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   6276 gaatctctcgagaacaagacggagctgtgtccctaccccgagcctgtgtctcggggggag 6335

QY   301 ctcttcgattctcgtggccgaagaagagtcactgagtgagagagagagccaccagcttcat 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   6336 ctcttcgactctccgtggcggagaagagtgctgcgacggagagagccaccagctcttc 6395

QY   361 aagcagatcctgtgagtgagtgaaactaccttcaacaagaagaattgtccacttcatatcc 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   6396 aagcagatcctgtgagcgcgttctactactcctgcagcactcaagcagcatcgcaacttgaactg 6455

QY   421 aag 423
    |||
DB   6456 aag 6458

Search completed: May 18, 2002, 02:17:48
Job time: 15052 sec

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